



## SEQUENCE LISTING

&lt;110&gt; Mount Sinai School of Medicine of NYU

<120> TRP8, A TRANSIENT RECEPTOR POTENTIAL  
CHANNEL EXPRESSED IN TASTE RECEPTOR CELL

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&lt;140&gt; 09/834,792

&lt;141&gt; 2001-04-13

&lt;150&gt; 60/197,491

&lt;151&gt; 2000-04-17

&lt;160&gt; 4

&lt;170&gt; Windows 2000 MS DOS w/ line breaks

&lt;210&gt; 1

&lt;211&gt; 4157

&lt;212&gt; DNA

&lt;213&gt; Murine TRP8 cDNA

&lt;400&gt; 1

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 Val Asp Ala Leu Val Ser Asn Lys Pro Glu Phe Val Arg Leu Phe Val  
 385 390 395 400  
 Asp Asn Gly Ala Asp Val Ala Asp Phe Leu Thr Tyr Gly Arg Leu Gln  
 405 410 415  
 Glu Leu Tyr Arg Ser Val Ser Arg Lys Ser Leu Leu Phe Asp Leu Leu  
 420 425 430  
 Gln Arg Lys Gln Glu Glu Ala Arg Leu Thr Leu Ala Gly Leu Gly Thr  
 435 440 445  
 Gln Gln Ala Arg Glu Pro Pro Ala Gly Pro Pro Ala Phe Ser Leu His  
 450 455 460  
 Glu Val Ser Arg Val Leu Lys Asp Phe Leu Gln Asp Ala Cys Arg Gly  
 465 470 475 480  
 Phe Tyr Gln Asp Gly Arg Pro Gly Asp Arg Arg Arg Ala Glu Lys Gly  
 485 490 495  
 Pro Ala Lys Arg Pro Thr Gly Gln Lys Trp Leu Leu Asp Leu Asn Gln  
 500 505 510  
 Lys Ser Glu Asn Pro Trp Arg Asp Leu Phe Leu Trp Ala Val Leu Gln  
 515 520 525  
 Asn Arg His Glu Met Ala Thr Tyr Phe Trp Ala Met Gly Gln Glu Gly  
 530 535 540  
 Val Ala Ala Ala Leu Ala Ala Cys Lys Ile Leu Lys Glu Met Ser His  
 545 550 555 560  
 Leu Glu Thr Glu Ala Glu Ala Ala Arg Ala Thr Arg Glu Ala Lys Tyr  
 565 570 575  
 Glu Arg Leu Ala Leu Asp Leu Phe Ser Glu Cys Tyr Ser Asn Ser Glu  
 580 585 590

Ala Arg Ala Phe Ala Leu Leu Val Arg Arg Asn Arg Cys Trp Ser Lys  
595 600 605  
Thr Thr Cys Leu His Leu Ala Thr Glu Ala Asp Ala Lys Ala Phe Phe  
610 615 620  
Ala His Asp Gly Val Gln Ala Phe Leu Thr Arg Ile Trp Trp Gly Asp  
625 630 635 640  
Met Ala Ala Gly Thr Pro Ile Leu Arg Leu Leu Gly Ala Phe Leu Cys  
645 650 655  
Phe Ala Leu Val Tyr Thr Asn Leu Ile Thr Phe Ser Glu Glu Ala Pro  
660 665 670  
Leu Arg Thr Gly Leu Glu Asp Leu Gln Asp Leu Asp Ser Leu Asp Thr  
675 680 685  
Glu Lys Ser Pro Leu Tyr Gly Leu Gln Ser Arg Val Glu Glu Leu Val  
690 695 700  
Glu Ala Pro Arg Ala Gln Gly Asp Arg Gly Pro Arg Ala Val Phe Leu  
705 710 715 720  
Leu Thr Arg Trp Arg Lys Phe Trp Gly Ala Pro Val Thr Val Phe Leu  
725 730 735  
Gly Asn Val Val Met Tyr Phe Ala Phe Leu Phe Leu Phe Thr Tyr Val  
740 745 750  
Leu Leu Val Asp Phe Arg Pro Pro Gln Gly Pro Ser Gly Pro Glu  
755 760 765  
Val Thr Leu Tyr Phe Trp Val Phe Thr Leu Val Leu Glu Glu Ile Arg  
770 775 780  
Gln Gly Phe Phe Thr Asp Glu Asp Thr His Leu Val Lys Lys Phe Thr  
785 790 795 800  
Leu Tyr Val Gly Asp Asn Trp Asn Lys Cys Asp Met Val Ala Ile Phe  
805 810 815  
Leu Phe Ile Val Gly Val Thr Cys Arg Met Leu Pro Ser Ala Phe Glu  
820 825 830  
Ala Gly Arg Thr Val Leu Ala Met Asp Phe Met Val Phe Thr Leu Arg  
835 840 845  
Leu Ile His Ile Phe Ala Ile His Lys Gln Leu Gly Pro Lys Ile Ile  
850 855 860  
Val Val Glu Arg Met Met Lys Asp Val Phe Phe Phe Leu Phe Phe Leu  
865 870 875 880  
Ser Val Trp Leu Val Ala Tyr Gly Val Thr Thr Gln Ala Leu Leu His  
885 890 895  
Pro His Asp Gly Arg Leu Glu Trp Ile Phe Arg Arg Val Leu Tyr Arg  
900 905 910  
Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro Leu Asp Glu Ile Asp Glu  
915 920 925  
Ala Arg Val Asn Cys Ser Thr His Pro Leu Leu Leu Glu Asp Ser Pro  
930 935 940  
Ser Cys Pro Ser Leu Tyr Ala Asn Trp Leu Val Ile Leu Leu Leu Val  
945 950 955 960  
Thr Phe Leu Leu Val Thr Asn Val Leu Leu Met Asn Leu Leu Ile Ala  
965 970 975  
Met Phe Ser Tyr Thr Phe Gln Val Val Gln Gly Asn Ala Thr Met Phe  
980 985 990  
Trp Lys Phe Gln Arg Tyr Asn Leu Ile Val Glu Tyr His Glu Arg Pro  
995 1000 1005  
Ala Leu Ala Pro Pro Phe Ile Leu Leu Ser His Leu Ser Leu Thr Leu  
1010 1015 1020  
Arg Arg Val Phe Lys Lys Glu Ala Glu His Lys Arg Glu His Leu Glu  
1025 1030 1035 1040  
Arg Asp Leu Pro Asp Pro Leu Asp Gln Lys Val Val Thr Trp Glu Thr  
1045 1050 1055

C1  
cut



Val Gln Lys Glu Asn Phe Leu Ser Lys Met Glu Lys Arg Arg Arg Asp  
 1060 1065 1070  
 Ser Glu Gly Glu Val Leu Arg Lys Thr Ala His Arg Val Asp Phe Ile  
 1075 1080 1085  
 Ala Lys Tyr Leu Gly Gly Leu Arg Glu Gln Glu Lys Arg Ile Lys Cys  
 1090 1095 1100  
 Leu Glu Ser Gln Ile Asn Tyr Cys Ser Val Leu Val Ser Ser Val Ala  
 1105 1110 1115 1120  
 Asp Val Leu Ala Gln Gly Gly Gly Pro Arg Ser Ser Gln His Cys Gly  
 1125 1130 1135  
 Glu Gly Ser Gln Leu Val Ala Ala Asp His Arg Gly Gly Ile Asp Gly  
 1140 1145 1150  
 Trp Glu Gln Pro Gly Ala Gly Gln Pro Pro Ser Asp Thr  
 1155 1160 1165